

SEQUENCE LISTING

<110> Kufer, et al.

<120> Heteromimibodies

<130> 009848/027 6371

<140> 09/744,625

<141> 2001-07-16

<150> EP 98 11 4082.5

<151> 1998-07-28

<160> 39

<170> PatentIn Ver. 2.1

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natural origin

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natural origin

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natural origin

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<211> 34

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<223> Description of Artificial Sequence: synthetic, no
natural origin

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natural origin

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ttcc 64

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natural origin

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<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 8

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<223> Description of Artificial Sequence: synthetic, no natural origin

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<210> 11
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<210> 12
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natural origin

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<212> DNA
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<400> 14
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<212> DNA
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natural origin

<400> 15
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<210> 16
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<210> 17
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natural origin

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<210> 18

<211> 18
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<400> 18
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18

<210> 19
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<400> 19
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<210> 20
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<210> 21
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36

A/C = M
A/G = R
G/C = S
A/T = W

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<212> DNA
<213> Artificial Sequence

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ccag 64

<210> 23
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<210> 24
<211> 29
<212> DNA
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<210> 25
<211> 67
<212> DNA
<213> Artificial Sequence

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cattgag 67

<210> 26
<211> 796
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (11) . . (793)

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gct aca ggt gta cac tcc gat atc gtt gtg act cag gaa tct gca ctc Ala Thr Gly Val His Ser Asp Ile Val Val Thr Gln Glu Ser Ala Leu	15 20 25	97
acc aca tca cct ggt gaa aca gtc aca ctc act tgt cgc tca agt act Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Thr	30 35 40 45	145
ggg gct gtt aca act agt aac tat gcc aac tgg gtc caa gaa aaa cca Gly Ala Val Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro	50 55 60	193
gat cat tta ttc act ggt cta ata ggt ggt acc aac aac cga gtt cca Asp His Leu Phe Thr Gly Leu Ile Gly Gly Thr Asn Asn Arg Val Pro	65 70 75	241
ggg gtt cct gcc aga ttc tca ggc tcc ctg att gga gac aag gct gcc Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala	80 85 90	289
ctc acc atc aca ggg gca cag act gag gat gag gca ata tat ttc tgt Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys	95 100 105	337
gct cta tgg tac agc aac cat tgg gtg ttc ggt gga gga acc aaa ctc Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly Thr Lys Leu	110 115 120 125	385
gag gtc cta ggt ggt ggt tct ggc ggc ggc tcc ggt ggt ggt Glu Val Leu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly	130 135 140	433
ggt tct cag gtc cag ctg cag gag tct gga cct ggc ctg gtg gcg ccc Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro	145 150 155	481
tca cag agc ctg tcc atc aca tgc acc atc tca ggg ttc tca tta act Ser Gln Ser Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu Thr	160 165 170	529
aag tat ggt gta cac tgg gtt cgc cag cct cca gga aag ggt ctg gag Lys Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu	175 180 185	577
tgg ctg gtg ata tgg act gat gga ggc aca tcc tat aat tca gct Trp Leu Val Val Ile Trp Thr Asp Gly Gly Thr Ser Tyr Asn Ser Ala	190 195 200 205	625
ctc aaa tcc aga ctg agc atc agc aag gac aac tcc aag agc caa gtt Leu Lys Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val	210 215 220	673
ttc tta aaa atg aac agt ctccaa act gat gac aca gcc atg tac tac Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr	225 230 235	721
tgt gcc aga cag gat aga tac gac ggt gga att gct tac tgg ggc caa Cys Ala Arg Gln Asp Arg Tyr Asp Gly Gly Ile Ala Tyr Trp Gly Gln	240 245 250	769

ggg acc acg gtc acc gtc tcc tcc gga
Gly Thr Thr Val Thr Val Ser Ser
255 260

796

<210> 27
<211> 261
<212> PRT
<213> Mus musculus

<400> 27
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20 25 30

Pro Gly Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val
35 40 45

Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu
50 55 60

Phe Thr Gly Leu Ile Gly Gly Thr Asn Asn Arg Val Pro Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile
85 90 95

Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp
100 105 110

Tyr Ser Asn His Trp Val Phe Gly Gly Thr Lys Leu Glu Val Leu
115 120 125

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
130 135 140

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu Thr Lys Tyr Gly
165 170 175

Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
180 185 190

Val Ile Trp Thr Asp Gly Gly Thr Ser Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
225 230 235 240

Gln Asp Arg Tyr Asp Gly Gly Ile Ala Tyr Trp Gly Gln Gly Thr Thr
245 250 255

Val Thr Val Ser Ser
260

<210> 28
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic, no natural origin

<400> 28
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<210> 29
 <211> 42
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: synthetic, no natural origin

<400> 29
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<210> 30
 <211> 1371
 <212> DNA
 <213> Homo sapiens/Mus musculus

<220>
 <221> CDS
 <222> (10)..(1359)

<400> 30
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 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala
 1 5 10

aca ggt gta cac tcc gat atc cag ctg acc cag tct caa aaa ttc atg 99
 Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Gln Lys Phe Met
 15 20 25 30

tcc aca tca gta gga gac agg gtc agc gtc acc tgc aag gcc agt cag 147
 Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln
 35 40 45

aat gtg ggt act aat gta gcc tgg tat caa cag aaa cca ggg caa tct 195
 Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
 50 55 60

cct aaa gca ctg att tac tcg gca tcc tac cgg tac agt gga gtc cct 243
 Pro Lys Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro
 65 70 75

gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc atc 291
 Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

80	85	90	
agc aat gtg cag tct gaa gac ttg gca gag tat ttc tgt cag caa tat Ser Asn Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr 95 100 105 110			339
aac agc tat ccg ctc acg ttc ggt gct ggg acc aag ctc gag atc aaa Asn Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys 115 120 125			387
ggt ggt ggt tct ggc ggc ggc tcc ggt ggt ggt tct cag Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Gln 130 135 140			435
gtg aaa ctg cag gag tca gga cct ggc cta gtg cag ccc tca cag agc Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser 145 150 155			483
ctg tcc atc acc tgc aca gtc tct ggt ttc tca tta act agc tat ggt Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly 160 165 170			531
gta cac tgg gtt cgc cag tct cca gga aag ggt ctg gag tgg ctg gga Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly 175 180 185 190			579
gtg ata tgg agt ggt gga agc aca gac tat aat gca gct ttc ata tcc Val Ile Trp Ser Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser 195 200 205			627
aga ctg agc atc agc aag gac aat tcc aag agc caa gtt ttc ttt aaa Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys 210 215 220			675
atg aac agt ctg caa gct aat gac aca gcc ata tat tac tgt gcc aga Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg 225 230 235			723
atg gag aac tgg tcg ttt gct tac tgg ggc caa ggg acc acg gtc acc Met Glu Asn Trp Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr 240 245 250			771
gtc tcc gaa ttc ccc aaa cct agc acc ccc cct ggc agc agt ggt gaa Val Ser Glu Phe Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Glu 255 260 265 270			819
ctg gaa gag ctg ctt aag cat ctt aaa gaa ctt ctg aag ggc ccc cgc Leu Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys Gly Pro Arg 275 280 285			867
aaa ggc gaa ctc gag gaa ctg ctg aaa cat ctg aag gag ctg ctt aaa Lys Gly Glu Leu Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys 290 295 300			915
ggt ggg agc gga ggc gcg ccg gca cct act tca agt tct aca aag aaa Gly Gly Ser Gly Gly Ala Pro Ala Pro Thr Ser Ser Thr Lys Lys 305 310 315			963
aca cag cta caa ctg gag cat tta ctg ctg gat tta cag atg att ttg Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu 320 325 330			1011

aat gga att aat aat tac aag aat ccc aaa ctc acc agg atg ctc aca Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr 335 340 345 350	1059
ttt aag ttt tac atg ccc aag aag gcc aca gaa ctg aaa cat ctt cag Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln 355 360 365	1107
tgt cta gaa gaa gaa ctc aaa cct ctg gag gaa gtg cta aat tta gct Cys Leu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala 370 375 380	1155
caa agc aaa aac ttt cac tta aga ccc agg gac tta atc agc aat atc Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile 385 390 395	1203
aac gta ata gtt ctg gaa cta aag gga tct gaa aca aca ttc atg tgt Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys 400 405 410	1251
gaa tat gct gat gag aca gca acc att gta gaa ttt ctg aac aga tgg Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp 415 420 425 430	1299
att acc ttt tgt caa agc atc atc tca aca ctg act gac gtc cat cac Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Asp Val His His 435 440 445	1347
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<210> 31
<211> 450
<212> PRT
<213> Homo sapiens/Mus musculus

<400> 31
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Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 50 55 60
Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg 65 70 75 80
Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn 85 90 95
Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser 100 105 110

Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Lys
130 135 140

Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser
145 150 155 160

Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His
165 170 175

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile
180 185 190

Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu
195 200 205

Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn
210 215 220

Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Met Glu
225 230 235 240

Asn Trp Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
245 250 255

Glu Phe Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Glu Leu Glu
260 265 270

Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys Gly Pro Arg Lys Gly
275 280 285

Glu Leu Glu Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys Gly Gly
290 295 300

Ser Gly Gly Ala Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
305 310 315 320

Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
325 330 335

Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
340 345 350

Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
355 360 365

Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
370 375 380

Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
385 390 395 400

Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
405 410 415

Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
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Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Asp Val His His His

435

440

445

His His
450

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<210> 32
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<213> Homo sapiens/Mus musculus
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<220>
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<222> (10) .. (1377)

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175 180 185 190	
gtg ata tgg agt ggt gga agc aca gac tat aat gca gct ttc ata tcc	627
Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser	
195 200 205	
aga ctg agc atc agc aag gac aat tcc aag agc caa gtt ttc ttt aaa	675
Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys	
210 215 220	
atg aac agt ctg caa gct aat gac aca gcc ata tat tac tgt gcc aga	723
Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg	
225 230 235	
atg gag aac tgg tcg ttt gct tac tgg ggc caa ggg acc acg gtc acc	771
Met Glu Asn Trp Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr	
240 245 250	
gtc tcc gaa ttc acc ccg ctg ggt gac acc acc cac acc tcc gga aaa	819
Val Ser Glu Phe Thr Pro Leu Gly Asp Thr Thr His Thr Ser Gly Lys	
255 260 265 270	
cca ctg gat gga gaa tat ttc acc ctt cag atc cgt ggg cgt gag cgc	867
Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg	
275 280 285	
ttc gag atg ttc cga gag ctg aat gag gcc ttg gaa ctc aag gat gcc	915
Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala	
290 295 300	
cag gct ggg aag gag cca ggg ggg agc gga ggc gcg ccg gca cct act	963
Gln Ala Gly Lys Glu Pro Gly Gly Ser Gly Ala Pro Ala Pro Thr	
305 310 315	
tca agt tct aca aag aaa aca cag cta caa ctg gag cat tta ctg ctg	1011
Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu	
320 325 330	
gat tta cag atg att ttg aat gga att aat aat tac aag aat ccc aaa	1059
Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys	
335 340 345 350	
ctc acc agg atg ctc aca ttt aag ttt tac atg ccc aag aag gcc aca	1107
Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr	
355 360 365	
gaa ctg aaa cat ctt cag tgt cta gaa gaa gaa ctc aaa cct ctg gag	1155
Glu Leu Lys His Leu Gln Cys Leu Glu Glu Leu Lys Pro Leu Glu	
370 375 380	
gaa gtg cta aat tta gct caa agc aaa aac ttt cac tta aga ccc agg	1203
Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg	
385 390 395	
gac tta atc agc aat atc aac gta ata gtt ctg gaa cta aag gga tct	1251
Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser	
400 405 410	
gaa aca aca ttc atg tgt gaa tat gct gat gag aca gca acc att gta	1299

Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val
 415 420 425 430

gaa ttt ctg aac aga tgg att acc ttt tgt caa agc atc atc tca aca 1347
 Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr
 435 440 445

ctg act gac gtc cat cac cat cac cat cac tgataagtcg ac 1389
 Leu Thr Asp Val His His His His His His
 450 455

<210> 33
 <211> 456
 <212> PRT
 <213> Homo sapiens/Mus musculus

<400> 33
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Val His Ser Asp Ile Gln Leu Thr Gln Ser Gln Lys Phe Met Ser Thr
 20 25 30

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val
 35 40 45

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
 50 55 60

Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg
 65 70 75 80

Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn
 85 90 95

Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser
 100 105 110

Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gln Val Lys
 130 135 140

Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser
 145 150 155 160

Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His
 165 170 175

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile
 180 185 190

Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu
 195 200 205

Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn
 210 215 220

Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Met Glu

225	230	235	240
Asn Trp Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser			
245	250	255	
Glu Phe Thr Pro Leu Gly Asp Thr Thr His Thr Ser Gly Lys Pro Leu			
260	265	270	
Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu			
275	280	285	
Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala			
290	295	300	
Gly Lys Glu Pro Gly Gly Ser Gly Gly Ala Pro Ala Pro Thr Ser Ser			
305	310	315	320
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu			
325	330	335	
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr			
340	345	350	
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu			
355	360	365	
Lys His Leu Gln Cys Leu Glu Glu Leu Lys Pro Leu Glu Glu Val			
370	375	380	
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu			
385	390	395	400
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr			
405	410	415	
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe			
420	425	430	
Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr			
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Asp Val His His His His His			
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 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala
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aca ggt gta cac tcc gat atc cag ctg acc cag cag tct cca gca atc atg 99

Thr	Gly	Val	His	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	
15					20				25					30		
tct	gca	tct	cca	ggg	gaa	aag	gtc	acc	atg	acc	tgc	agg	gcc	agc	tca	147
Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	
35								40						45		
agt	gtt	agt	tcc	agt	tac	ttg	cac	tgg	tac	cag	cag	aag	tca	ggt	gcc	195
Ser	Val	Ser	Ser	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Ala		
50								55						60		
tcc	ccc	aaa	ctc	tgg	att	tat	agc	aca	tcc	aac	ttg	gct	tct	gga	gtc	243
Ser	Pro	Lys	Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	
65								70						75		
cct	gct	cgc	ttc	agt	ggc	agt	ggg	tct	ggg	acc	tct	tac	tct	ctc	aca	291
Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	
80								85						90		
atc	agc	agt	gtg	gag	gct	gaa	gat	gct	gcc	act	tat	tac	tgc	cag	cag	339
Ile	Ser	Ser	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
95								100						105		110
tac	agt	ggt	tac	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctc	gag	atc	387
Tyr	Ser	Gly	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	
115								120						125		
aaa	ggg	ggg	ggg	ggg	tct	ggc	ggc	ggc	tcc	ggt	ggg	ggt	ggg	tct		435
Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
130								135						140		
cag	gtg	aaa	ctg	cag	gag	tct	ggg	gct	gag	ctt	gtg	aag	cct	ggg	gct	483
Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	
145								150						155		
tca	gtg	aag	ctg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ctc	acc	agc	tac	531
Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Leu	Thr	Ser	Tyr	
160								165						170		
tgg	ttg	cac	tgg	gtg	aag	cag	tgg	cct	gga	cga	ggc	ctt	gag	tgg	att	579
Trp	Leu	His	Trp	Val	Lys	Gln	Trp	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	
175								180						185		190
gga	agg	att	gat	ccc	aat	agt	ggt	act	aag	tac	gat	gag	aag	ttc		627
Gly	Arg	Ile	Asp	Pro	Asn	Ser	Gly	Gly	Thr	Lys	Tyr	Asp	Glu	Lys	Phe	
195								200						205		
aag	agc	aag	gcc	aca	ctg	act	gta	gac	aaa	ccc	tcc	agc	aca	gcc	tac	675
Lys	Ser	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Pro	Ser	Ser	Thr	Ala	Tyr	
210								215						220		
atg	cag	ctc	agc	agc	ctg	aca	tct	gag	gac	tct	gcg	gtc	tat	tat	tgt	723
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
225								230						235		
gca	aga	tgg	gac	tac	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tcc	771
Ala	Arg	Trp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
240								245						250		
gga	acc	ccg	ctg	ggt	gac	acc	acc	cac	act	agt	gga	aaa	cca	ctg	gat	819
Gly	Thr	Pro	Leu	Gly	Asp	Thr	Thr	His	Thr	Ser	Gly	Lys	Pro	Leu	Asp	

255	260	265	270	
gga gaa tat ttc acc ctt cag atc cgt ggg cgt gag cgc ttc gag atg Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu Met				867
275	280		285	
tcc cga gag ctg aat gag gcc ttg gaa ctc aag gat gcc cag gct ggg Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala Gly				915
290	295		300	
aag gag cca ggg ggg tcc gga ggt ggt ggt agc acc caa gtg tgc acc Lys Glu Pro Gly Gly Ser Gly Gly Ser Thr Gln Val Cys Thr				963
305	310		315	
ggc aca gac atg aag ctg cgg ctc cct gcc agt ccc gag acc cac ctg Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu				1011
320	325		330	
gac atg ctc cgc cac ctc tac cag ggc tgc cag gtg gtg cag gga aac Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn				1059
335	340		345	
350				
ctg gaa ctc acc tac ctg ccc acc aat gcc agc ctg tcc ttc ctg cag Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln				1107
355	360		365	
gat atc cag gag gtg cag ggc tac gtg ctc atc gct cac aac caa gtg Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val				1155
370	375		380	
agg cag gtc cca ctg cag agg ctg cgg att gtg cga ggc acc cag ctc Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu				1203
385	390		395	
ttt gag gac aac tat gcc ctg gcc gtg cta gac aat gga gac ccg ctg Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu				1251
400	405		410	
aac aat acc acc cct gtc aca ggg gcc tcc cca gga ggc ctg cgg gag Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu				1299
415	420		425	
430				
ctg cag ctt cga agc ctc aca gag atc ttg aaa gga ggg gtc ttg atc Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile				1347
435	440		445	
cag cgg aac ccc cag ctc tgc tac cag gac acg att ttg tgg aag gac Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp				1395
450	455		460	
atc ttc cac aag aac aac cag ctg gct ctc aca ctg ata gac acc aac Ile Phe His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn				1443
465	470		475	
cgc tct cgg gcc tgc cac ccc tgt tct ccg atg tgt aag ggc tcc cgc Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg				1491
480	485		490	
tgc tgg gga gag agt tct gag gat tgt cag agc ctg acg cgc act gtc Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val				1539
495	500		505	
				510

tgt gcc ggt ggc tgt gcc cgc tgc aag ggg cca ctg ccc act gac tgc Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys 515 520 525	1587
tgc cat gag cag tgt gct gcc ggc tgc acg ggc ccc aag cac tct gac Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp 530 535 540	1635
tgc ctg gcc tgc ctc cac ttc aac cac agt ggc atc tgt qag ctg cac Cys Leu Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His 545 550 555	1683
tgc cca gcc ctg gtc acc tac aac aca gac acg ttt gag tcc atg ccc Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro 560 565 570	1731
aat ccc gag ggc cg ^g tat aca ttc ggc gcc agc tgt gtg act gcc tgt Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys 575 580 585 590	1779
ccc tac aac tac ctt tct acg gac gtg gga tcc tgc acc ctc gtc tgc Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys 595 600 605	1827
ccc ctg cac aac caa gag gtg aca gca gag gat gga aca cag cgg tgt Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys 610 615 620	1875
gag aag tgc agc aag ccc tgt gcc cga gtg tgc tat ggt ctg ggc atg Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met 625 630 635	1923
gag cac ttg cga gag gtg agg gca gtt acc agt gcc aat atc cag gag Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu 640 645 650	1971
ttt gct ggc tgc aag aag atc ttt ggg agc ctg gca ttt ctg ccg gag Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu 655 660 665 670	2019
agc ttt gat ggg gac cca gcc tcc aac act gcc ccg ctc cag cca gag Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu 675 680 685	2067
cag ctc caa gtg ttt gag act ctg gaa gag atc aca ggt tac cta tac Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr 690 695 700	2115
atc tca gca tgg ccg gac agc ctg cct gac ctc agc gtc ttc cag aac Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn 705 710 715	2163
ctg caa gta atc cgg gga cga att ctg cac aat ggc gcc tac tcg ctg Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu 720 725 730	2211
acc ctg caa ggg ctg ggc atc agc tgg ctg ggg ctg cgc tca ctg agg Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg 735 740 745 750	2259

gaa ctg ggc agt gga ctg gcc ctc atc cac cat aac acc cac ctc tgc Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys	755	760	765	2307	
ttc gtg cac acg gtg ccc tgg gac cag ctc ttt cg ^g aac cc ^g cac caa Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln	770	775	780	2355	
gct ctg ctc cac act gcc aac cc ^g cca gag gac gag t ^t gt ggc gag Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu	785	790	795	2403	
ggc ctg gcc tgc cac cag ctg tgc gcc cga ggg cac tgc tgg ggt cca Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro	800	805	810	2451	
ggg ccc acc cag t ^t gt gtc aac tgc agc cag ttc ctt cg ^g ggc cag gag Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu	815	820	825	830	2499
tgc gtg gag gaa tgc cga gta ctg cag ggg ctc ccc agg gag tat gtg Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val	835	840	845	2547	
aat gcc agg cac t ^t gt ttg cc ^g tgc cac cct gag t ^t gt cag ccc cag aat Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn	850	855	860	2595	
ggc tca gtg acc t ^t gt ttt gga cc ^g gag gct gac cag t ^t gt gtc g ^c cc t ^t gt Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys	865	870	875	2643	
gcc cac tat aag gac cct ccc ttc tgc gtg gcc cgc tgc ccc agc ggt Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly	880	885	890	2691	
gtg aaa cct gac ctc tcc tac atg ccc atc tgg aag ttt cca gat gag Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu	895	900	905	910	2739
gag ggc gca tgc cag cct tgc ccc atc aac tgc acc cac tcc t ^t gt gtg Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val	915	920	925	2787	
gac ctg gat gac aag ggc tgc ccc gcc gag cag aga gcc agc cct ctg Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu	930	935	940	2835	
acg tcc ggg cat cat cac cat cat cat tgagtcgac Thr Ser Gly His His His His His His	945	950		2871	

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Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
35 40 45

Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro
50 55 60

Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95

Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser
100 105 110

Gly Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
130 135 140

Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val
145 150 155 160

Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Ser Tyr Trp Leu
165 170 175

His Trp Val Lys Gln Trp Pro Gly Arg Gly Leu Glu Trp Ile Gly Arg
180 185 190

Ile Asp Pro Asn Ser Gly Gly Thr Lys Tyr Asp Glu Lys Phe Lys Ser
195 200 205

Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr Met Gln
210 215 220

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Trp Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr
245 250 255

Pro Leu Gly Asp Thr Thr His Thr Ser Gly Lys Pro Leu Asp Gly Glu
260 265 270

Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu Met Phe Arg
275 280 285

Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala Gly Lys Glu
290 295 300

Pro Gly Gly Ser Gly Gly Ser Thr Gln Val Cys Thr Gly Thr
305 310 315 320

Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
325 330 335

Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
340 345 350

Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
355 360 365

Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
370 375 380

Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
385 390 395 400

Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
405 410 415

Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
420 425 430

Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
435 440 445

Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
450 455 460

His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
465 470 475 480

Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
485 490 495

Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
500 505 510

Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
515 520 525

Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
530 535 540

Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
545 550 555 560

Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
565 570 575

Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
580 585 590

Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu
595 600 605

His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys
610 615 620

Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His
625 630 635 640

Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala
645 650 655

Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe

660	665	670
Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu		
675	680	685
Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser		
690	695	700
Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln		
705	710	715
Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu		
725	730	735
Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu		
740	745	750
Gly Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val		
755	760	765
His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu		
770	775	780
Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu		
785	790	795
800		
Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro		
805	810	815
Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val		
820	825	830
Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala		
835	840	845
Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser		
850	855	860
Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His		
865	870	875
880		
Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys		
885	890	895
Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly		
900	905	910
Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu		
915	920	925
Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser		
930	935	940
Gly His His His His His		
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<222> (39)..(1607)

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Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Leu Gln
10 15 20

atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc 152
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
25 30 35

acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat tgg 200
Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
40 45 50

tat cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg gca 248
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
55 60 65 70

tct acc cgg gaa tcc ggg gtc cct gac cga ttc agc ggc agt gaa tct 296
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Glu Ser
75 80 85

ggg aca aat tac act ctc acc atc agc agc ctg cag cct gaa gat ttt 344
Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
90 95 100

gct act tac ttt tgt caa cag tct gac agt ttg ccg atc acc ttc ggc 392
Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser Leu Pro Ile Thr Phe Gly
105 110 115

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Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly Ser Gly Gly Gly
120 125 130

ggt agc ggc ggc ggc tca gag gtg cag ctg ctc gag tct ggg gga 488
Gly Ser Gly Gly Ser Glu Val Gln Leu Leu Ser Gly Gly Gly
135 140 145 150

ggc gtg gtc cag cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct 536
Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
155 160 165

gga ttc acc ttc agt agc tat ggc atg cac tgg gtc cgc cag gct cca 584
Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro
170 175 180

ggc aag ggg ctg gag tgg gtg gca gtt ata tca tat gat gga agt aat 632
Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn
185 190 195

aaa tac tat gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac 680
Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

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acg gtc acc gtc tcc tcc gga acc ccg ctg ggt gac acc acc cac acc Thr Val Thr Val Ser Ser Gly Thr Pro Leu Gly Asp Thr Thr His Thr 265 270 275			872
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ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr 345 350 355			1112
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aat gcc atc cag gag gcc cgg cgt ctc ctg aac ctg agt aga gac act Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr 410 415 420			1304
gct gct gag atg aat gaa aca gta gaa gtc atc tca gaa atg ttt gac Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp 425 430 435			1352
ctc cag gag ccg acc tgc cta cag acc cgc ctg gag ctg tac aag cag Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln 440 445 450			1400

ggc ctg cgg ggc agc ctc acc aag ctc aag ggc ccc ttg acc atg atg		1448
Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met		
455	460	465
		470
gcc agc cac tac aag cag cac tgc cct cca acc ccg gaa act tcc tgt		1496
Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys		
475	480	485
gca acc cag att atc acc ttt gaa agt ttc aaa gag aac ctg aag gac		1544
Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp		
490	495	500
ttt ctg ctt gtc atc ccc ttt gac tgc tgg gag cca gtc cag gag cat		1592
Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu His		
505	510	515
cat cac cat cat cat tgagtgcact taaaacagct ctg		1630
His His His His		
520		

<210> 37						
<211> 523						
<212> PRT						
<213> Homo sapiens/Mus musculus						
<400> 37						
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly						
1	5	10		15		
Val His Ser Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala						
20	25		30			
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile						
35	40		45			
Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys						
50	55		60			
Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg						
65	70		75		80	
Phe Ser Gly Ser Glu Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser						
85		90		95		
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser						
100		105		110		
Leu Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly						
115		120		125		
Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Glu Val Gln						
130		135		140		
Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg						
145		150		155		160
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His						
165		170			175	

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
180 185 190

Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
210 215 220

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp
225 230 235 240

Met Gly Trp Gly Ser Gly Trp Arg Pro Tyr Tyr Tyr Gly Met Asp
245 250 255

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Pro Leu
260 265 270

Gly Asp Thr Thr His Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
275 280 285

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
290 295 300

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
305 310 315 320

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
325 330 335

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
340 345 350

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
355 360 365

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
370 375 380

Ser Gly Gly Gly Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr
385 390 395 400

Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu
405 410 415

Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val
420 425 430

Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
435 440 445

Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys
450 455 460

Gly Pro Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro
465 470 475 480

Thr Pro Glu Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe
485 490 495

Lys Glu Asn Leu Lys Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp

500

505

510

Glu Pro Val Gln Glu His His His His His His
 515 520

<210> 38

<211> 1630

<212> DNA

<213> Homo sapiens/Mus musculus

<220>

<221> CDS

<222> (39) ..(1610)

<400> 38

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 Met Gly Trp Ser Cys Ile
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atc ctc ttc ttg gta gca aca gct aca ggt gta cac tcc gag ctc cag 104
 Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Leu Gln
 10 15 20

atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc 152
 Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 25 30 35

acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat tgg 200
 Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
 40 45 50

tat cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg gca 248
 Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 55 60 65 70

tct acc cgg gaa tcc ggg gtc cct gac cga ttc agc ggc agt gaa tct 296
 Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Glu Ser
 75 80 85

ggg aca aat tac act ctc acc atc agc agc ctg cag cct gaa gat ttt 344
 Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 90 95 100

gct act tac ttt tgt caa cag tct gac agt ttg ccg atc acc ttc ggc 392
 Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser Leu Pro Ile Thr Phe Gly
 105 110 115

caa ggg aca cga ctg gac att caa gga gga gga tca ggt ggt ggt 440
 Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly Gly Ser Gly Gly Gly
 120 125 130

ggt agc ggc ggc ggc tca gag gtg cag ctg ctc gag tct ggg gga 488
 Gly Ser Gly Gly Ser Gly Val Gln Leu Leu Glu Ser Gly Gly
 135 140 145 150

ggc gtg gtc cag cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct 536
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
 155 160 165

gga ttc acc ttc agt agc tat ggc atg cac tgg gtc cgc cag gct cca Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro	584
170 175 180	
ggc aag ggg ctg gag tgg gtg gca gtt ata tca tat gat gga agt aat Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn	632
185 190 195	
aaa tac tat gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp	680
200 205 210	
aat tcc aag aac acg ctg tat ctg caa atg aac agc ctg aga gct gag Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu	728
215 220 225 230	
gac acg gct gtg tat tac tgt gcg aaa gat atg ggg tgg ggc agt ggc Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Met Gly Trp Gly Ser Gly	776
235 240 245	
tgg aga ccc tac tac tac tac ggt atg gac gtc tgg ggc caa ggg acc Trp Arg Pro Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr	824
250 255 260	
acg gtc acc gtc tcc tcc gga acc ccg ctg ggt gac acc acc cac acc Thr Val Thr Val Ser Ser Gly Thr Pro Leu Gly Asp Thr Thr His Thr	872
265 270 275	
cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu	920
280 285 290	
cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe	968
295 300 305 310	
tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln	1016
315 320 325	
tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser	1064
330 335 340	
acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu	1112
345 350 355	
aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser	1160
360 365 370	
ccc gtc aca aag agc ttc aac agg gga gag tgt tca gga ggc ggt ggg Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser Gly Gly Gly	1208
375 380 385 390	
tct gca cct act tca agt tct aca aag aaa aca cag cta caa ctg gag Ser Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu	1256
395 400 405	
cat tta ctg ctg gat tta cag atg att ttg aat gga att aat aat tac	1304

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr			
410	415	420	
aag aat ccc aaa ctc acc agg atg ctc aca ttt aag ttt tac atg ccc			1352
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro			
425	430	435	
aag aag gcc aca gaa ctg aaa cat ctt cag tgt cta gaa gaa gaa ctc			1400
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu			
440	445	450	
aaa cct ctg gag gaa gtg cta aat tta gct caa agc aaa aac ttt cac			1448
Lys Pro Leu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His			
455	460	465	470
tta aga ccc agg gac tta atc agc aat atc aac gta ata gtt ctg gaa			1496
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu			
475	480	485	
cta aag gga tct gaa aca aca ttc atg tgt gaa tat gct gat gag aca			1544
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr			
490	495	500	
gca acc att gta gaa ttt ctg aac aga tgg att acc ttt tgt caa agc			1592
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser			
505	510	515	
atc atc tca aca cta act tgataagtgc acttaaaaca			1630
Ile Ile Ser Thr Leu Thr			
520			

<210> 39
<211> 524
<212> PRT
<213> Homo sapiens/Mus musculus

<400> 39			
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
Val His Ser Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala			
20	25	30	
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile			
35	40	45	
Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys			
50	55	60	
Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg			
65	70	75	80
Phe Ser Gly Ser Glu Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser			
85	90	95	
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser			
100	105	110	
Leu Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly			
115	120	125	

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
130 135 140

Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
180 185 190

Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
210 215 220

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp
225 230 235 240

Met Gly Trp Gly Ser Gly Trp Arg Pro Tyr Tyr Tyr Tyr Gly Met Asp
245 250 255

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Pro Leu
260 265 270

Gly Asp Thr Thr His Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile
275 280 285

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
290 295 300

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
305 310 315 320

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
325 330 335

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
340 345 350

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
355 360 365

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
370 375 380

Cys Ser Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
385 390 395 400

Thr Gln Leu Gln Leu Glu His Leu Leu Asp Leu Gln Met Ile Leu
405 410 415

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
420 425 430

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
435 440 445

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
450 455 460

Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
465 470 475 480

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
485 490 495

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
500 505 510

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
515 520